RAW SEQUENCE LISTING

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Application Serial Number: 10/625, 204

Source: JFWOO

Date Processed by STIC: 06/14/ 2005

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RAW SEQUENCE LISTING   DATE: 06/14/2005
PATENT APPLICATION: US/10/625,204   TIME: 14:02:14

Input Set : **A:\89DIV1.ST25.txt**
Output Set: **N:\CRF4\06142005\J625204.raw**

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 3 <110> APPLICANT: Figdor, Carl Gustav
 4        Geijtenbeek, Teunis Bernard Herman
 5        Van Kooyk, Yvette
 6        Torensma, Ruurd
 8 <120> TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING DENDRITIC CELL-T CELL
 9        INTERACTION
11 <130> FILE REFERENCE: 89 DIV
13 <140> CURRENT APPLICATION NUMBER: US/10/625,204
14 <141> CURRENT FILING DATE: 2003-07-23
16 <150> PRIOR APPLICATION NUMBER: 09/719,961
17 <151> PRIOR FILING DATE: 2001-09-24
19 <150> PRIOR APPLICATION NUMBER: PCT/NL00/00253
20 <151> PRIOR FILING DATE: 2000-04-19
22 <150> PRIOR APPLICATION NUMBER: US 60/176,924
23 <151> PRIOR FILING DATE: 2000-01-20
25 <150> PRIOR APPLICATION NUMBER: EP 99201204.7
26 <151> PRIOR FILING DATE: 1999-04-19
28 <160> NUMBER OF SEQ ID NOS: 2
30 <170> SOFTWARE: PatentIn version 3.2
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1215
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (1)..(1215)
42 <400> SEQUENCE: 1
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44 Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu Glu
45 1               5                   10                  15
47 gag gaa cag ctg aga ggc ctt gga ttc cga cag act cga gga tac aag      96
48 Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys
49              20                  25                  30
51 agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc     144
52 Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu
53          35                  40                  45
55 tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc     192
56 Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro
57      50                  55                  60
59 agc tcc ata agt cag gaa caa tcc agg caa gac gcg atc tac cag aac     240
60 Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn
61 65                  70                  75                  80
63 ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca gag aaa tcc aag     288
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64 Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys
65                   85                  90                  95
67 ctg cag gag atc tac cag gag ctg acc cag ctg aag gct gca gtg ggt      336
68 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly
69                  100                 105                 110
71 gag ctt cca gag aaa tct aag ctg cag gag atc tac cag gag ctg acc      384
72 Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
73             115                 120                 125
75 cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag ctg cag      432
76 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
77       130                 135                 140
79 gag atc tac cag gag ctg acc tgg ctg aag gct gca gtg ggt gag ctt      480
80 Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu
81 145                 150                 155                 160
83 cca gag aaa tct aag atg cag gag atc tac cag gag ctg act cgg ctg      528
84 Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
85                 165                 170                 175
87 aag gct gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc      576
88 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile
89            180                 185                 190
91 tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ctt cca gag      624
92 Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
93             195                 200                 205
95 aaa tct aag cag cag gag atc tac cag gag ctg acc cgg ctg aag gct      672
96 Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala
97       210                 215                 220
99 gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc tac cag      720
100 Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
101 225                 230                 235                 240
103 gag ctg acc cag ctg aag gct gca gtg gaa cgc ctg tgc cac ccc tgt     768
104 Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys
105                 245                 250                 255
107 ccc tgg gaa tgg aca ttc ttc caa gga aac tgt tac ttc atg tct aac     816
108 Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn
109                 260                 265                 270
111 tcc cag cgg aac tgg cac gac tcc atc acc gcc tgc aaa gaa gtg ggg     864
112 Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly
113             275                 280                 285
115 gcc cag ctc gtc gta atc aaa agt gct gag gag cag aac ttc cta cag     912
116 Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln
117       290                 295                 300
119 ctg cag tct tcc aga agt aac cgc ttc acc tgg atg gga ctt tca gat     960
120 Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
121 305                 310                 315                 320
123 cta aat cag gaa ggc acg tgg caa tgg gtg gac ggc tca cct ctg ttg     1008
124 Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
125                 325                 330                 335
127 ccc agc ttc aag cag tat tgg aac aga gga gag ccc aac aac gtt ggg     1056
128 Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
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129                 340                 345                 350
131 gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg aac gac gac aaa      1104
132 Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys
133         355                 360                 365
135 tgt aat ctt gcc aaa ttc tgg atc tgc aaa aag tcc gca gcc tcc tgc      1152
136 Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys
137     370                 375                 380
139 tcc agg gat gaa gaa cag ttt ctt tct cca gcc cct gcc acc cca aac      1200
140 Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn
141 385                 390                 395                 400
143 ccc cct cct gcg tag                                                  1215
144 Pro Pro Pro Ala
148 <210> SEQ ID NO: 2
149 <211> LENGTH: 404
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 2
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159 Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys
160             20                  25                  30
163 Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu
164         35                  40                  45
167 Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro
168     50                  55                  60
171 Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn
172 65                  70                  75                  80
175 Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys
176             85                  90                  95
179 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly
180             100                 105                 110
183 Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
184         115                 120                 125
187 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
188     130                 135                 140
191 Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu
192 145                 150                 155                 160
195 Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
196             165                 170                 175
199 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile
200             180                 185                 190
203 Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
204         195                 200                 205
207 Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala
208     210                 215                 220
211 Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
212 225                 230                 235                 240
215 Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys
216             245                 250                 255
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219 Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn
220         260             265             270
223 Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly
224         275             280             285
227 Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln
228         290             295             300
231 Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
232 305             310             315             320
235 Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
236             325             330             335
239 Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
240         340             345             350
243 Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys
244         355             360             365
247 Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys
248         370             375             380
251 Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn
252 385             390             395             400
255 Pro Pro Pro Ala
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/625,204

DATE: 06/14/2005
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Input Set : A:\89DIV1.ST25.txt
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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number